



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 169358

TO: Patricia Duffy
Art Unit: 1645
Location: REM-3B05/3C18
Serial Number: 09/880748

Monday, November 07, 2005

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

Patricia,

Over 20K hits were saved. However, when the dup removal command was executed, all 20K hits were retained.

Your seq. results files were saved via the WinZip format. They are labeled as follows:

- *RAG.ZIP (File RAG)
- *COMM.ZIP (Files RPR, RUP, RAI and RAPB)
- *PEND.ZIP (Files RAPM and RAPN)

If you experience any probs. w/ the disks, pls. contact me.

Beverly

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.



Multi-Dup Searches

(07/12/05)

This search is designed as a work-around when search results are cluttered with matches from multiple related cases sharing the same sequence disclosure. A special procedure for processing these cases has been developed to help examiners find sequence matches that are not part of the related group. Depending on the database searched, the procedure either removes the duplicate cases from the answer set, or allows for the easy identification of related applications. In accordance with this procedure, the search is processed as follows:

1. Published Applications files:

Save 1500 hits, 0 alignments. A post-processing script is run to remove multiple cases sharing identical disclosures of the same sequence leaving only one case per group of identical disclosures remaining in the results set.

2. Geneseq:

Save 1500 hits, 1500 alignments. A post-processing script removes **all** of the alignments but leaves abbreviated citation information, which allows easy identification of the related cases.

3. Issued Patents and Commercial files other than Geneseq:

Save 1500 hits, 15 alignments. No post-processing is done.

If you need detailed information about how the post-processing script works when applied to the results in 1 or 2 above, please contact David Schreiber.

4. Pending Files

The pending file search is to determine if there are other application(s) which interfere with the application being examined. Pending files are to be searched only when all claims being examined are allowable.

If you need to have the pending files searched, please e-mail your search request to Michael Woodward, Bonnie Eyler or Tony Caputa to get their approval for a pending file search. The Library will not process a pending file search request without their approval. Please note that pending file searches should normally only be requested as part of the interference search at time of allowance.

Requesting Alignments not Supplied in Original Result Set

(04/25/05)

To request alignments for specific hits from this answer set, e-mail the searcher who processed the original search request for this case and include the following information:

1. The serial number and the sequence ID number from your case and
2. Identifying data for the sequence(s) for which you would like an alignment.

The identifying data can be **ONE** of the following:

- In the Issued and Published Applications files: **Serial number and Sequence ID number**
- In the GenEMBL and EST files: the **alphanumeric character string** in the **Accession** or **Locus** field (e.g. BC000000).
- In the Geneseq files: the **alphanumeric character string** in the **ID** field (e.g. AAV00000)

Example:

The original multi-dup search was on Seq ID 100 from 00/000000.

You now need to see alignments for this sequence with Result No. 458 from the GeneSeq file, which is AXY00000 and with Result 325 from the Issued file.

Please give your alignment request as shown below:

Please align Seq ID 100 from 00/000000 with the following sequences:

AXY00000	Geneseq	(the ID data for result 458 in Geneseq)
XX/000,000-Seq XX	Issued	(the ID data for result 325 in the Issued file)

Do **NOT** use the original Results Number to identify the sequences needing to be aligned, but please do provide the database name. The searcher will contact you if the identifying data is insufficient.

STIC-Biotech/ChemLib

Twelve (12) disks
169558

LB

From: Duffy, Patricia
Sent: Wednesday, October 26, 2005 8:56 AM
To: STIC-Biotech/ChemLib
Subject: afterfinal sequence search
Importance: High

CRFE

Dear stic, I need the following sequences searched. PLEASE HAVE THE SEARCHER CALL ME BEFORE PERFORMING THE PROTEIN SEARCH. THIS CASE AS 10,000 HIGHLY RELATED SEQUENCES WHICH WE NEED TO GET BEHIND TO VIEW POTENTIAL ART.

In re: 09/880,748

- Please search AA residues 1-123 of SEQ ID NO:327. *aa 249*
Please search AA residues 141-249 of SEQ ID NO:327.
Please search AA residues 1-123 of SEQ ID NO:2.
Please search AA residues 141-249 of SEQ ID NO:2. *aa 249*
Please include both a commercial database and interference search.

Patricia A. Duffy, Ph.D.
Art Unit 1645
Remsen 3B05; Mailbox 3C18
571-272-0855

CPDI

7127

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

Date completed: _____
Searcher: *Beverly e 2528*
Terminal time: _____
Elapsed time: _____
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site
____ STIC
____ CM-1
____ Pre-S
Type of Search
____ N.A. Sequence
____ A.A. Sequence
____ Structure
____ Bibliographic

Vendors
____ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ ☒ Other *CGN*